

## Theme session K

### New approaches to the understanding of energy transfer through the food webs

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The energy transfers within the ocean food webs are complex and sometimes difficult to fully comprehend. The topic of energy transfer has, therefore, been a focus of sessions on several occasions during previous ICES science conferences. At each session, new jigsaw pieces reveal more about the complex food web of the ocean. It is also clear that there is a constant evolution of new or refined techniques to fully understand the food web. The importance of better understanding the energy flow is multidimensional, as it can serve directives such as the Marine Strategy Framework Directive or the Water Framework Directive, while also driving better use and management of the sea. The methods used range from hands-on analyses of gut content of larger organisms, to more refined visual aids for the smaller organisms, to models to try to grasp the large and complex overall picture.

The function and energy flow of lower trophic levels of the food web has its obstacles to understand. The small size of these organisms limits the applications of more traditional ways to elucidate the energy transfer, such as gut contents analysis. Nevertheless, these small organisms play a vital role in the energy transfer efficiency of the food web. Two presentations described the use of new techniques to reveal the energy transfer. A study of the selectivity and preference of microzooplankton herbivory was presented using flow cytometry and FlowCam in a grazing experiment, where micro- and mesozooplankton fed on natural phytoplankton communities; the species composition before and after feeding sessions were analyzed (Fileman et al.) Another presentation showed the use of an autonomous Video Plankton Recorder to study the prey preference of lower trophic levels. This study showed interesting interactions between different zooplankton, such as the harpacticoid copepod *Microsetella norvegica*, different calanoid copepod nauplii, and polychaete larvae. These were associated with aggregates formed from diatom chains, Phaeocystis colonies, and fecal pellets. The results presented a successful way of revealing new interactions, where both marine snow and fecal pellets play an important role in the energy flow (Norrbin et al.).

Combining methods can offer new insights into feeding ecology. Several studies in this session used a combination of techniques, i.e. morphological taxonomy of the gut content, carbon and nitrogen stable isotope analysis, and/or molecular methods (DNA metabarcoding) to address energy flow through the food webs (Bucklin et al., Mavraki et al, Bachiller et al. and Rodríguez-Ezpeleta et al.). Bucklin et al. reported results of integrative molecular methods (DNA metabarcoding), morphological stomach content analyses, and stable isotope analyses of the diet and trophic position of salps and mesopelagic fishes from the slope water of the Northwest Atlantic Ocean. Molecular DNA metabarcoding analysis is useful for classifying prey which are difficult to identify by morphological taxonomic methods. Compound-specific stable isotope analysis of the salp

tunic yielded new understanding in trophic relationship of salps, including the tracing of the food chain back to the biological source. DNA metabarcoding analysis of the gut content of the mesopelagic fishes led to results that were comparable with those from the morphological taxonomic analysis. Lamb et al. concluded that jellyfish predation might be more common than previously acknowledged; they conducted a molecular gut content assessment of 50 potential predators of jellyfish in the Irish Sea using cnidarian-specific mtDNA primers and sequencing. Mavraki et al. used both stomach content analysis, carbon and nitrogen stable isotope analysis, and a stable isotope mixing model to study diet and overlap between the trophic niches of five fish species related to an offshore wind farm at the Belgian part of the North Sea. The results presented showed that fouling amphipods and decapods were an important food source for fish inside the offshore wind farm area. The combination of visual characterization and DNA metabarcoding analyses of the stomach content of anchovy and sardine suggests a latitudinal trend in the Northwest Mediterranean pelagic ecosystem, with higher feeding success in the southern area. The studies by Rodríguez-Ezpeleta et al. on the diet of five commercially important fish species allowed them to define guidelines for studying trophic interactions, and for the integration of metabarcoding-based diet data into ecosystem models.

The session finished with a series of modelling studies, showing how Ecopath models can be used to analyze energy flow and trophic structure of pelagic food webs. For example, Surma et al. showed that using energy-balanced rather than mass-balanced food web models can help to better understand ecosystem structure and trophodynamics. This is particularly helpful in food webs with species that store large amounts of lipid, such as herring in northern British Columbia. In subsequent discussion it was argued that resolving high energy and low energy phytoplankton and zooplankton groups may also significantly improve model predictions. Han et al. used Ecopath to compare recent and former ecosystem status, reveal control mechanisms (e.g. the impact of top down control), and discuss a potential maturation of the ecosystem structure. Both studies indicate that careful parametrization and a comprehensive dataset is usually a necessary premise for this kind of modelling. This can be a significant challenge, especially when historic changes need to be resolved. Planque et al. addressed this issue, using a 'Chance and Necessity' (CaN) modelling approach, which accounts for input and output uncertainties while also allowing an assessment of trophic flows even if the data on several trophic groups are unavailable.

This session highlighted to an impressive degree the wide variety of methods that have been used to address similar questions about energy flows. It also revealed that while, as expected, all methods have their own advantages and drawbacks as well as a different taxonomical and timely resolution, most methods have seen methodological improvements and progress in recent years. This is true not only for molecular methods but also optical methods; modelling approaches also benefit from rapid developments in computational power, allowing better and more precise estimations of trophic links in the pelagic food web.